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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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EXAMINER	
FREDMAN, JEFFREY NORMAN	
ART UNIT	PAPER NUMBER
1637	

DATE MAILED: 09/05/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/032,281	WYRICK ET AL.	
	Examiner	Art Unit	
	Jeffrey Fredman	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *July 20, 2006*.

2a)☒ This action is **FINAL**. 2b)☐ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-6,8-11,15-26,28-43,45-59 and 61-92* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-6,8-11,15-26,28-43,45-59 and 61-92* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☐ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date 8/06.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other: _____.

DETAILED ACTION

Claim Rejections - 35 USC § 103

1. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

2. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

3. Claims 1-6, 8, 10, 11, 17-22, 39-43, 45, 48-53, 56-59, 61, 64-68, 71-76, 78-84 and 87-92 are rejected under 35 U.S.C. 103(a) as being unpatentable over Orlando et al (Methods (1997) 11:205-214) in view of Schena (Tibtech (1998) 16:301-306).

Orlando teaches a method of claims 1, 10, 11 and 71 for identifying a region of a genome of a cell to which a protein of interest binds (see abstract) comprising the steps of:

a) crosslinking DNA binding proteins in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA (see figure 1 and page 205-206, subheading "1. In vivo Formaldehyde fixation of cells"),

b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound (see figure 1 and page 206, subheading "2. Chromatin solubilization by sonication"),

c) removing a DNA fragment to which the protein of interest is bound from the mixture produced in b) (see figure 1 and page 209, subheading "5. Immunoprecipitation of crosslinked chromatin"),

d) separating the DNA fragment identified in c) from the protein of interest (see figure 1 and page 210, subheading "6. Reversal of cross-links and DNA purification"),

e) amplifying the DNA fragment of d) (see figure 1 and page 210-211, subheading "8. Amplification of immunoprecipitated DNA by linker modified DNA PCR"),

f) combining the DNA fragment of e) with DNA comprising more than one sequence complementary to more than one intergenic regions of genomic DNA of the cell under conditions in which hybridization between the DNA fragments and a sequence complementary to an intergenic region of the genomic DNA occurs (see figure 1 and subheading "9. southern analysis and mapping of binding sites in DNA" where the figures 6 and 7 demonstrate that multiple sequences of multiple intergenic regions are on the blot as shown by the presence of probes such as probe 2206 which is between the ultrabithorax and abdominal-A genes),

g) identifying the one or more sequences complementary to the one or more intergenic regions of genomic DNA of f) to which the DNA fragment hybridizes whereby the region identified in g) is the region of the genome in the cell to which the protein of interest binds (see figure 1, page 211, column 2 and figures 6 and 7).

With regard to claims 1, 10, 11 and 71, Orlando teaches hybridization to a southern blot, which is a type of microarray as discussed above (see figure 6).

With regard to claims 2, 39, 56, 72, Orlando teaches the use of Drosophila melanogaster cells which are eukaryotic (see page 205, column 1).

With regard to claims 3, 40, Orlando teaches the use of DNA binding transcription factors (see page 213, column 2).

With regard to claims 4, 41, 57, 73, Orlando teaches crosslinking with formaldehyde (see page 205-206, subheading "1. In vivo Formaldehyde fixation of cells").

With regard to claims 5, 42, 58, 74, Orlando teaches the use of antibodies to bind the protein of interest (see page 209, subheading "5. Immunoprecipitation of crosslinked chromatin").

With regard to claims 6, 43, 59, 75, 90 and 91, Orlando teaches the use of a ligation mediated PCR since the linkers must be ligated prior to PCR (see page 210-211, subheading "8. Amplification of immunoprecipitated DNA by linker modified DNA PCR").

With regard to claims 8, 45, 61, 76, Orlando teaches the use of a control (see figure 7, figure legend "The white bars indicate the fragments containing repetitive elements (M-repeats) that hybridized also with the control fraction").

With regard to claims 17, 48, 64, 79, Orlando teaches shearing the DNA to make fragments (see page 206, subheading "2. Chromatin solubilization by sonication").

With regard to claims 18-22, 49-53, 65-68, 80-84, Orlando teaches the entire upstream and downstream regions of the abdominal-A gene which inherently includes promoter and regulatory regions for abdominal-A and abdominal-B.

With regard to claims 87, Orlando teaches identifying a DNA binding site of the protein where the protein is a transcription factor (see figure 1, page 211, column 2 and figures 6 and 7).

Orlando does not teach substitution of a DNA microarray with specific spots for the Southern blot used for detection in step (f).

Schena teaches the use of microarrays to analyze genomic information (see abstract).

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to substitute the microarrays of Schena for the Southern blot of Orlando since Schena expressly notes "Although reminiscent of filter based assays, chip assays are a fundamental departure from techniques that employ porous membranes. Chips allow true parallelism, miniaturization, multiplexing and automation, and these key features provide a set of performance specifications that cannot be achieved with the earlier technologies (see page 301, column 2)." Schena is expressly

teaching that chip assays are superior to the prior art filter based assays such as Southern blots of Orlando. Schena provides significant additional motivation to use microarrays in the place of such filter based assays noting,

> "Microarray assays allow massive parallel data acquisition and analysis. Parallelism greatly increases the speed of experimental progress and allows meaningful comparisons to be made between the genes or gene products represented in the microarray. Microarray assays may eventually allow the analysis of the entire human genome in a single reaction, and recent gene-expression experiments in yeast represent an important step towards this goal. Miniaturization of conventional assays is a general trend in biomedical research. Microscale assays reduce reagent consumption, minimize reaction volumes, increase the sample concentration and accelerate the reaction kinetics. Chip-based assays allow sensitive and rapid data detection with either confocal scanners or cameras equipped with charged-coupled devices. Although current microarray assays focus on nucleic acid hybridization, future studies will undoubtedly involve the parallel analysis of proteins, lipids, carbohydrates and small molecules. Multiplexing, the process by which multiple samples are analysed in a single assay, is another enabling feature of the microarray approach. Novel labelling and detection methods, such those involving multicolour fluorescence, allow comparisons of multiple samples to be made on a single chip. Multiplexing increases the accuracy of comparative analysis by eliminating complicating factors such as chip-to-chip variation, discrepancies in reaction conditions and other shortcomings inherent in comparing separate experiments (see page 301-302)."

An ordinary practitioner, motivated by Orlando to analyze genomic nucleic acids in order to identify regions of protein binding, would have been motivated by Schena to substitute the use of a microarray for the southern blot since Schena teaches that microarrays are faster, provide more meaningful comparisons, reduce reagent consumption and accelerate reaction kinetics, as well as increasing accuracy as discussed by Schena above.

Further, it would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to apply the method of Orlando the entire genome, as required by claims 88, 89 and 92, in order to analyze the location of transcription factors on the entire genome simultaneously. This is particularly obvious in light of Schena, who teaches analysis of genomic samples.

4. Claims 1-6, 8-11, 15-22, 25, 26, 28-36, 39-53, 56-59, 61-68, 71-84 and 87-92 are rejected under 35 U.S.C. 103(a) as being unpatentable over Mercola (U.S. Patent 6,410,233) in view of Schena (Tibtech (1998) 16:301-306).

Mercola teaches a method of claims 1, 9, 10 and 11 for identifying a region of a genome of a cell to which a protein of interest binds (see abstract) comprising the steps of:

a) crosslinking DNA binding proteins in the cell to genomic DNA of the cell, thereby producing DNA binding protein crosslinked to genomic DNA (see figure 1),

b) generating DNA fragments of the genomic DNA crosslinked to DNA binding protein in a), thereby producing a mixture comprising DNA fragments to which DNA binding protein is bound (see figure 1),

c) removing a DNA fragment to which the protein of interest is bound from the mixture produced in b) (see figure 1),

d) separating the DNA fragment identified in c) from the protein of interest (see figure 1),

e) amplifying the DNA fragment of d) (see figure 1),

f) combining the DNA fragment of e) with DNA comprising sequences complementary to intergenic regions of genomic DNA of the cell under conditions in which hybridization between the DNA fragments and a sequence complementary to an intergenic region of the genomic DNA occurs (see figure 1),

g) identifying the one or more sequences complementary to the one or more intergenic regions of genomic DNA of f) to which the DNA fragment hybridizes whereby the region identified in g) is the region of the genome in the cell to which the protein of interest binds (see figure 1).

Mercola expressly states "For example, a region of a nucleic acid molecule that binds with a transcription factor can be within a gene, upstream of a gene or downstream of a gene (see column 14, lines 48-50)." The only reasonable interpretation of Mercola's teaching of regions "upstream" or "downstream" of a gene is regions that by definition are between genes and therefore "intergenic". Mercola therefore expressly teaches intergenic regions.

With regard to claims 1, 10, 11 and 71, Mercola teaches hybridization to cDNAs on a matrix (see figure 1), which is an express form of a microarray.

With regard to claims 9, 15, 16, 29-30, 46, 47, 62, 63, 77, 78, Mercola teaches the use of fluorescent labels such as Cy3 and Cy5 (see column 17, lines 60-65).

With regard to claims 2, 25, 39, 56, 72, Mercola teaches the use of cells which are eukaryotic (see column 11, line 23).

With regard to claims 3, 26, 40, Mercola teaches the use of DNA binding transcription factors (see column 11, line 6).

With regard to claims 4, 41, 57, 73, Mercola teaches crosslinking with formaldehyde (see figure 1).

With regard to claims 5, 42, 58, 74, Mercola teaches the use of antibodies to bind the protein of interest (see figure 1).

With regard to claims 6, 43, 59, 75, 90 and 91Mercola teaches the use of a ligation mediated PCR since the linkers must be ligated prior to PCR (see figure 1).

With regard to claims 8, 28, 45, 61, 76, Mercola teaches the use of a control (see column 19, lines 23-25).

With regard to claims 17, 31, 48, 64, 79, Mercola teaches shearing the DNA to make fragments (see figure 1).

With regard to claims 18-22, 49-53, 65-68, 80-84, Mercola teaches the analysis of the Egr-1 transcription factor control elements and genes (see example 1) where "EGR1 belongs to a group of proteins that are involved in the progress through G1 phase of the cell cycle (see http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=eurekah.section.11998).

With regard to claims 87-89 and 92, Mercola expressly teaches the desirability of genomic DNA (see column 11, lines 5-10 and claim 3, which expressly recite genomic DNA).

Mercola does not teach substitution of a DNA microarray with specific spots for the matrix used for detection in step (f).

Schena teaches the use of microarrays to analyze genomic information (see abstract).

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to substitute the microarrays of Schena for the blot of Mercola since Schena expressly notes "Although reminiscent of filter based assays, chip assays are a fundamental departure from techniques that employ porous membranes. Chips allow true parallelism, miniaturization, multiplexing and automation, and these key features provide a set of performance specifications that cannot be achieved with the earlier technologies (see page 301, column 2)." Schena is expressly teaching that chip assays are superior to the prior art filter based assays such as blots of Mercola. Schena provides significant additional motivation to use microarrays in the place of such filter based assays noting,

> "Microarray assays allow massive parallel data acquisition and analysis. Parallelism greatly increases the speed of experimental progress and allows meaningful comparisons to be made between the genes or gene products represented in the microarray. Microarray assays may eventually allow the analysis of the entire human genome in a single reaction, and recent gene-expression experiments in yeast represent an important step towards this goal. Miniaturization of conventional assays is a general trend in biomedical research. Microscale assays reduce reagent consumption, minimize reaction volumes, increase the sample concentration and accelerate the reaction kinetics. Chip-based assays allow sensitive and rapid data detection with either confocal scanners or cameras equipped with charged-coupled devices. Although current microarray assays focus on nucleic acid hybridization, future studies will undoubtedly involve the parallel analysis of proteins, lipids, carbohydrates and small molecules. Multiplexing, the process by which multiple samples are analysed in a single assay, is another enabling feature of the microarray approach. Novel labelling and detection methods, such those involving multicolour fluorescence, allow comparisons of multiple samples to be made on a single chip. Multiplexing increases the accuracy of comparative analysis by eliminating complicating factors such as chip-to-chip variation, discrepancies in reaction

> conditions and other shortcomings inherent in comparing separate experiments (see page 301-302)."

An ordinary practitioner, motivated by Mercola to analyze genomic nucleic acids in order to identify regions of protein binding, would have been motivated by Schena to substitute the use of a microarray for the southern blot since Schena teaches that microarrays are faster, provide more meaningful comparisons, reduce reagent consumption and accelerate reaction kinetics, as well as increasing accuracy as discussed by Schena above.

5. Claims 9, 15, 16, 25, 26, 28-36, 46, 47, 62, 63, 77 and 78 are rejected under 35 U.S.C. 103(a) as being unpatentable over Orlando et al (Methods (1997) 11:205-214) in view of Schena (Tibtech (1998) 16:301-306) and further in view of Hacia et al (Nucleic Acids Research (1998) 26(16):3865-3866).

Orlando in view of Schena teach the limitations of claims 1-6, 8, 10, 11, 17-22, 39-43, 45, 48-53, 56-59, 61, 64-68, 71-76 and 78-84 as discussed above.

While Orlando does not teach the use of fluorescent labels, Schena expressly teaches the use of multicolor fluorescence for detection (see page 302). However, neither teaches the use of Cy5.

Hacia teaches the use of a two label system where one of the labels is Cy5-phycoerythrin (see page 3865, column 2).

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to substitute the fluorescent Cy5 dye of Hacia into the detection method of Orlando in view of Schena since the use of fluorescent dyes permits replacement of the radioactive components used in Orlando and avoidance of radioactivity is desirable. Further motivation to use the Cy5 dye of Hacia is provided by Hacia, who notes "An attractive aspect of this two color system is the minimal spectral overlap between the phycoerythrin and phycoerythrin-Cy5 dyes (see page 3866, column 2)." Hacia notes that "Two color analysis allows competitive hybridization between a reference standard and an unknown sample, improving the performance of the assay (see abstract)." So an ordinary practitioner, wishing to modify Orlando in view of Schena in order to solve Orlando's concern regarding background and specificity (see page 213, column 1, where Orlando is seriously concerned with background signal in the hybridization), would have been motivated to use the two color system of Hacia since the two color system would improve signal specificity and accuracy as taught by Hacia (see page 3866, column 2). Further motivation to use Cy5 is that minimal spectral overlap is imposed when this dye is used in combination with phycoerythrin as discussed by Hacia.

6. Claims 23, 24, 37, 38, 54, 55, 69, 70, 85 and 86 are rejected under 35 U.S.C. 103(a) as being unpatentable over Orlando et al (Methods (1997) 11:205-214) in view of Schena in view of Hacia et al (Nucleic Acids Research (1998) 26(16):3865-3866) and further in view of Hallahan et al (J. Biol. Chem. (1995) 270(51):30303-9).

Orlando in view of Schena and further in view of Hacia teach the limitations of claims 1-11, 15-22, 25-36, 39-53 and 56-68 as discussed above.

In particular, Orlando clearly teaches that the method of analysis is generic, noting "We have substantially broadened the potential of the method by adapting it to the analysis of general transcription factors (see page 205, column 2)."

Orlando in view of Schena and further in view of Hacia do not teach the species of cell cycle transcription factors.

Hallahan teach the analysis of transcription factors that are associated with cell cycle and in particular, analyzed the G1, S and G2/M transitions (see page 30304, column 2).

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to apply the method of Orlando in view of Schena and further in view of Hacia to any transcription factor, including cell cycle transcription factors such as those of Hallahan since Orlando notes "We have substantially broadened the potential of the method by adapting it to the analysis of general transcription factors (see page 205, column 2)." An ordinary practitioner would have been motivated to use the method of Orlando to study the transcription factors of Hallahan in order to determine where the transcription factors bind on the genomic DNA, in order to determine the higher order structure which controls gene transcription of these cell cycle factors of Hallahan.

7. Claims 23, 24, 37, 38, 54, 55, 69, 70, 85 and 86 are rejected under 35 U.S.C. 103(a) as being unpatentable over Mercola (U.S. Patent 6,410,233) in view of Schena and further in view of Hallahan et al (J. Biol. Chem. (1995) 270(51):30303-9).

Mercola in view of Schena teaches the limitations of claims 1-11, 15-22, 25-36, 39-53 and 56-68 as discussed above. Mercola teaches the analysis of the Egr-1 transcription factor control elements and genes (see example 1) where "EGR1 belongs to a group of proteins that are involved in the progress through G1 phase of the cell cycle (see http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=eurekah.section.11998).

Mercola does not teach the species of cell cycle transcription factors.

Hallahan teach the analysis of transcription factors that are associated with cell cycle and in particular, analyzed the G1, S and G2/M transitions (see page 30304, column 2).

It would have been prima facie obvious to one of ordinary skill in the art at the time the invention was made to apply the method of Mercola to any transcription factor, particularly cell cycle transcription factors such as those of Hallahan since an ordinary practitioner would have been motivated to use the method of Mercola to study the transcription factors of Hallahan in order to determine where the transcription factors bind on the genomic DNA, in order to determine the higher order structure which controls gene transcription of these cell cycle factors of Hallahan.

Double Patenting

8. The rejection of claims 1-6, 8-11 and 15-26, 28-43, 45-59 and 61-86 under the judicially created doctrine of obviousness-type double patenting as being unpatentable

over claims 1-11 of U.S. Patent No. 6,410,243 in view of Hacia and further in view of Hallahan is withdrawn in view of the terminal disclaimer.

Response to Arguments

9. Applicant's arguments filed March 9, 2006 have been fully considered but they are not persuasive.

Applicant has amended the claims to further define the fragments being analyzed on the microarray.

The claims now require "more than one intergenic region" and "more than one transcribed region". This modification does not affect the applicability of the Orlando reference since Orlando teaches sequences (as shown in figure 7), of three genes, ultrabithorax, abdominal-A and Abdominal-B, which represent three transcribed regions. These sequences are clearly "across a portion of the genome". Therefore, Orlando remains applicable and the rejection is maintained.

Applicant argues that Mercola does not teach "intergenic regions". This is not correct. Mercola expressly states "For example, a region of a nucleic acid molecule that binds with a transcription factor can be within a gene, upstream of a gene or downstream of a gene (see column 14, lines 48-50)." The only reasonable interpretation of Mercola's teaching of regions "upstream" or "downstream" of a gene is regions that by definition are between genes and therefore "intergenic". Mercola therefore expressly teaches intergenic regions.

Applicant relies upon overcoming these rejections to overcome the remaining 103 rejections. Since these rejections are maintained, so are the remaining 103 rejections.

Conclusion

10. Applicant's amendment necessitated the new ground(s) of rejection presented in this Office action. Accordingly, **THIS ACTION IS MADE FINAL**. See MPEP § 706.07(a). Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the date of this final action.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Jeffrey Fredman whose telephone number is (571)272-0742. The examiner can normally be reached on 6:30-3:00.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on (571)272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Jeffrey Fredman
Primary Examiner
Art Unit 1637
9/10/06